

Aberdeen Angus beef quality and profitability in dependence of the genotypes

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Abstract. The study of the influence of some candidate genes on beef cattle productivity has been conducted. The Aberdeen Angus bulls (n=9) of Russian population have been genotyped on leptin, calpain 1 and calpastatin gene polymorphisms by earlier developed own test systems based on PCR-RFLP and RT-PCR methods. The data of live weight, carcass weight and yield, content in the carcass of premium cuts, meat pulp, fat and trimming and broth bones have been registered. In addition, the profits of the sale of bulls' beef has been counted. The correlation analyses has shown the higher live weight and more content in the carcasses of premium cuts and meat pulp in beef obtained from animals of CC-Arg4Cys *LEP*, GG-*CAPNI_316*, TT-*CAPNI_4751*, GG-*CAST_282* and GG-*CAST_2959* genotypes. The cost of the sale of these animals' beef was also higher due more content of the most expensive cuts in their carcasses. We have concluded that the studied gene polymorphisms could be perspective genetic markers on meat productivity provided the conduction of the investigation of largescale correlation analysis of the allele variants with the phenotype appearances with the further study of the gene expression, confirming their significant influence on the beef production and quality.

1 Introduction

The increasing of the meat cattle profitability is the main priority task of the Russian agriculture [1]. The beef palatability plays the important role in the people consumption demand of beef [2]. There are many out and inner factors influenced on quality characteristics of cattle meat – animal feeding, managing, and slaughter and post slaughter conditions [3]. It has been noted that the carcass traits is difficult for the accession – we can make some conclusions only after animal slaughter [4]. Due this fact, the investigation of the gene influence the certain single nucleotide polymorphisms (SNP) on the beef properties is actual [5].

The leptin gene (*LEP*) of cattle codes the same namely protein playing the different functions in body. It is a hormone takes part in the appetite regulation, immune response and

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reproduction. The cattle LEP gene located on chromosome 4 (BTA 4) and counted about 60 polymorphisms the most significant of them is Arg4Cys LEP (R25C) [6, 7].

It's known that tenderness of meat directly influenced on beef palatability formed by proteins of calpain-calpastatin cascade [8].

Calpain 1 gene (*CAPN1*) located in cattle on BTA29 codes the most important protease participated in post mortem proteolysis of muscle fibers [9]. The main SNPs have been identified in this gene are in exon 9 CAPN1_316, (g.44069063C>G, rs17872000) and in exon 14 CAPN1_4751 (g.44087629C>T, rs17872050 [10]. The preferable in point of beef tenderness alleles are C-CAPN1_316 and C-CAPN1_4751 [11].

Calpastatin is the inhibitor of calpain protein [10], gene of which (*CAST*) located on BTA7 has length of 149 thousands base pairs and consists of 35 exons [12]. The most considerable SNP are CAST_282 (:g.98533961C>G, rs110955059) and CAST_2959 (g.98579663A>G, rs109221039) [13]. The desirable allele are C-CAST_282 and A-CAST_2959 [11].

The aim of our investigation was to evaluate of the association of different genotypes of polymorphisms of leptin (Arg4Cys LEP), calpain 1 (CAPN1_316, CAPN1_4751) and calpastatin (CAST_282, CAST_2959) genes with the carcass quality figures of beef cattle and profitability of animal selection with the determined genotypes.

2 Material and methods

As a research material were bulls (n=9) of Aberdeen Angus breed from the farm located in Kaluga region of Russia. The bulls were born in the period of March 2020-March 2021 and after fattening (from March to June of 2023) were slaughtered.

The data of live weight (kg), carcass weight (kg), slaughter yield (%) were registered. Also, the losses (kg) under the deboning and tenderization processes have been counted. The commercial carcass weight (kg) was calculated by carcass weight minus losses of deboning and tenderization. In addition, content in carcass of meat pulp (kg), cuts on the bone (kg), fat (kg), trimming (kg) and broth bones (kg) were collected.

The carcasses were divided into cuts (premium, meat pulp, fat and trimming and broth bones) and sold on the Russian market in Russian rubles (₽). The average realization prices were: premium cuts - ₽1575, meat pulp - ₽588, fat and trimming - ₽675 and broth bones - ₽263. The obtained profit of realization of the cuts of carcasses animals of the different genotypes of leptin, calpain 1 and calpastatin genes was evaluated.

For the DNA analysis the blood samples from the animals have been collected. The DNA preparation has been conducted by DNA-Extran 1 kits (Syntol Company, Russia) in according to the manufacturer's instructions.

The DNA probes has been analyzed on polymorphisms of leptin (*Arg4Cys*) [14], calpain 1 (*CAPN1_316*, *CAPN1_4751*) [14, 15] and calpastatin (*CAST_282*, *CAST_2959*) genes. For the analyses the polymerase chain reaction with the subsequent polymorphism length restriction fragments (PCR-RFLP) and real-time PCR (RT-PCR) methods have been chosen.

The calculation of the results and statistical analysis has been conducted by Microsoft Excel and Medical statistics software (https://medstatistic.ru/articles_science.html). For each genotype group the average mean (\bar{X}) and the square deviation (σ) of trait have been calculated and the significances of the differences between the groups have been evaluated by t-Student criterion (the differences have been considered as significant under $p < 0.05$).

3 Results

The genotyping of the bulls (Table 1) has shown the presence of the all possible genotypes of the studied polymorphisms of leptin, calpain 1 and calpastatin gene, excluding of CAST_282 – on this SNP the animals with GC- and GG-genotypes were present and carriers of CC-genotype were absent.

Table 1. The results of genotyping of the Aberdeen Angus bulls on the leptin (*LEP*), calpain 1 (*CAPN1*) and calpastatin (*CAST*) genes polymorphisms.

Bull No.	Genotype				
	<i>Arg4Cys LEP</i>	<i>CAPN1_316</i>	<i>CAPN1_4751</i>	<i>CAST_282</i>	<i>CAST_2959</i>
1	TT	GC	CT	GC	AA
2	TT	GG	CT	GC	AG
3	TT	CC	CC	GC	AG
4	CT	GC	CC	GG	AG
5	CT	GC	CT	GC	AG
6	CT	GG	CC	GG	GG
7	CC	GG	TT	GC	GG
8	CC	CC	CC	GC	AA
9	CC	GG	TT	GC	AG

The analysis of live and after slaughter weights of the bulls presented in Table 2.

Table 2. Live, before and after slaughter figures of the Aberdeen Angus bulls of the different leptin, calpain 1 and calpastatin genotypes.

SNP	Genotype (n)	Live weight, kg	Carcass weight, kg	Carcass yield, %	Commercial carcass weight, kg
Arg4Cys LEP	CC (3)	647.3±5.8	387.6±4.2	59.9±0.7	294.6±3.6
	CT (3)	639.0±6.6	382.9±5.5	59.9±0.8	293.4±5.5
	TT (3)	621.3±7.6	361.6±5.7	58.2±0.8	279.6±5.2
CAPN1_316	CC (2)	590.5±6.5	352.4±5.6	59.6±1.1	270.1±4.4
	GC (3)	635.7±6.2	375.9±4.5	59.2±1.0	288.0±4.7
	GG (4)	658.8±5.6	391.0±5.0	59.3±1.1	299.6±4.8
CAPN1_4751	CC (4)	624.5±7.2	374.7±5.9	60.0±0.9	288.5±5.4
	CT (3)	634.3±6.3	369.9±4.6	58.3±0.9	283.0±4.8
	TT (2)	661.0±5.8	394.0±4.4	59.6±0.3	299.8±3.7
CAST_282	GC (7)	629.4±6.6	371.8±5.1	59.1±1.0	284.1±4.5
	GG (2)	658.5±6.3	397.0±5.1	60.3±0.5	306.9±5.2
CAST_2959	AA (2)	648.5±6.3	384.7±3.7	59.4±1.2	297.0±4.3
	AG (5)	610.8±5.6	360.7±4.5	59.1±1.0	274.6±3.8
	GG (2)	686.0±1.2	411.7±2.3	60.0±0.8	317.8±3.4

The highest live weight has been observed in bulls with genotypes of CC-Arg4Cys LEP, GG-CAPN1_316, TT-CAPN1_4751, GG-CAST_282 and GG-CAST_2959 (Table 2). The carcass weights were highest in bulls of genotypes of CC-Arg4Cys LEP (387.6 kg against 361.6 kg of TT-genotype), GG-CAPN1_316 (391.0 kg – more on 38.6 kg compared with CC genotype), GG-CAPN1_4751 (more on 24.1 kg compared with GC-genotype), GG-CAST_282 (more on 29.1 kg compared with the heterozygous animals) and GG-CAST_2959 (more on 24.0 kg compared with AA-genotype). These results were statistically significant ($p < 0.05$). The carcass yields were relatively high in all animals (58.2-60.3%) and we have not observed any dependence of this figure from genotypes of the studied genes polymorphisms.

Despite of the higher losses of weight in animals of these genotypes due deboning and tenderization processes (Table 3) their commercial carcass weights were significantly higher.

Table 3. Weight losses of the Aberdeen Angus bulls' carcasses of the different leptin, calpain 1 and calpastatin genotypes.

SNP	Genotype (n)	Weight loss, kg due	
		Deboning	Tenderization
Arg4Cys LEP	CC (3)	81.0±2.0	12.0±1.2
	CT (3)	80.2±1.3	9.7±0.6
	TT (3)	72.4±2.4	9.5±1.4
CAPN1_316	CC (2)	73.2±3.2	9.0±1.4
	GC (3)	78.7±1.9	9.5±0.3
	GG (4)	79.6±2.0	11.8±1.2
CAPN1_4751	CC (4)	77.0±2.7	9.4±1.1
	CT (3)	76.7±1.4	10.2±1.1
	TT (2)	81.4±2.3	12.8±0.6
CAST_282	GC (7)	77.0±2.4	10.6±1.4
	GG (2)	80.8±1.4	9.7±0.6
CAST_2959	AA (2)	77.7±1.9	10.0±0.9
	AG (5)	76.1±2.5	10.1±1.4
	GG (2)	82.3±2.0	11.5±1.5

The analysis of the meat cutting data showed that in animals with the certain genotypes had highest weights of most valuable cuts (premium and meat pulp) compared with other allele variants (Table 4). Therefore, the carcasses of CC-Arg4Cys LEP-animals had more weight of premium, meat pulp, trimming and broth bones compared with other genotypes but less content of fat. Relating to CAPN1_316 polymorphism the same tendency has been observed – the GG-genotype carcasses contended less fat under high content of the rest figures. The carcasses of GG-CAST_282 and GG-CAST_2959 animals have shown the highest meanings of all figures.

Table 4. Composition of the Aberdeen Angus bulls' carcasses dependent of the *LEP*, *CAPNI* and *CAST* polymorphisms genotype.

SNP	Genotype (n)	Weight of cut, kg ($\bar{X} \pm \sigma$)				
		premium	meat pulp	fat	trimming	broth bones
Arg4Cys LEP	CC (3)	56.7±1.1	133.4±2.5	18.6±1.6	70.5±2.0	15.4±1.3
	CT (3)	55.6±3.1	128.2±3.5	20.7±0.8	74.2±2.5	14.7±1.4
	TT (3)	50.4±1.9	125.5±3.8	24.2±1.7	66.5±2.9	13.1±1.0
CAPNI_ 316	CC (2)	52.8±2.0	119.6±3.2	18.4±1.8	65.7±2.9	13.7±0.8
	GC (3)	51.6±1.7	128.4±3.6	22.4±1.9	72.4±1.9	13.1±0.9
	GG (4)	56.9±2.8	134.2±2.8	21.6±1.7	71.2±2.8	15.8±1.3
CAPNI_ 4751	CC (4)	56.0±2.7	127.0±3.4	19.7±1.6	71.3±3.0	14.5±1.3
	CT (3)	49.9±1.9	126.5±3.6	24.0±1.8	69.4±2.5	13.2±1.0
	TT (2)	57.1±1.1	136.8±1.8	19.9±1.4	70.0±2.3	16.0±1.4
CAST_ 282	GC (7)	52.8±2.1	127.5±3.4	21.2±1.9	68.5±2.4	14.1±1.3
	GG (2)	59.2±3.1	134.5±2.9	20.9±0.9	76.9±2.4	15.4±1.5
CAST_ 2959	AA (2)	55.0±1.0	134.0±3.2	21.3±2.7	73.6±1.8	13.1±1.2
	AG (5)	50.8±1.9	122.8±3.0	21.0±1.6	66.2±2.2	13.8±0.8
	GG (2)	62.1±2.4	139.6±1.0	21.4±0.3	77.5±2.3	17.2±0.5

The data of Figure 1 have visually confirmed data of Table 4. The carcasses of animals with CC-Arg4Cys *LEP* genotypes have contented more premium cuts (19.2% compared 18.9% – in CT and 18.0% in TT-genotypes) and meat pulp (45.3% compared 43.7% and 44.9% in CT- and TT-genotypes, respectively) with the smallest fat per cent – on 0.8% less than CT- and on 2.4% less that TT-genotypes.

For *CAPNI*_316 gene polymorphism we have observed the highest content of premium cuts in animals with CC-genotype (on 0.6% more than in GG- and on 1.7% than GC genotype), also these animals' carcasses had the smallest fat percent – less compared with GC- on 1.0% and GG – on 1.2%. The meat pulp content was a little higher in GG-carcasses. The analysis of *CAPNI*_4751 polymorphism has shown the same picture. Notably, that the part of broth bones were the smallest in the carcasses of heterozygous animals.

Unfortunately, on *CAST*_282 the bulls homozygous on C-allele were absent and so we have compared two genotypes - GC- and GG and could observed that the carcasses of GG-genotype-animals had better figures of premium cuts and trimming compared with GC-ones. In GC-carcasses the content of meat pulp was a little larger (on 1.1%) compared with GG-analogues. In the carcasses of both genotypes the content of broth bones was equal (5.0%).

On *CAST*_2959 we have observed the advantage in the share of premium cuts in GG-carcasses –on 1.0% larger compared with the heterozygous and homozygous on A-allele analogues. However, meat pulp content was the highest in AA-carcasses (45.1%>44.7%>43.9% in AA, AG, GG-genotypes). The fat content was the smallest in GG-carcasses (6.7% compared with 7.6 in AG and 7.2 in AA-genotype).

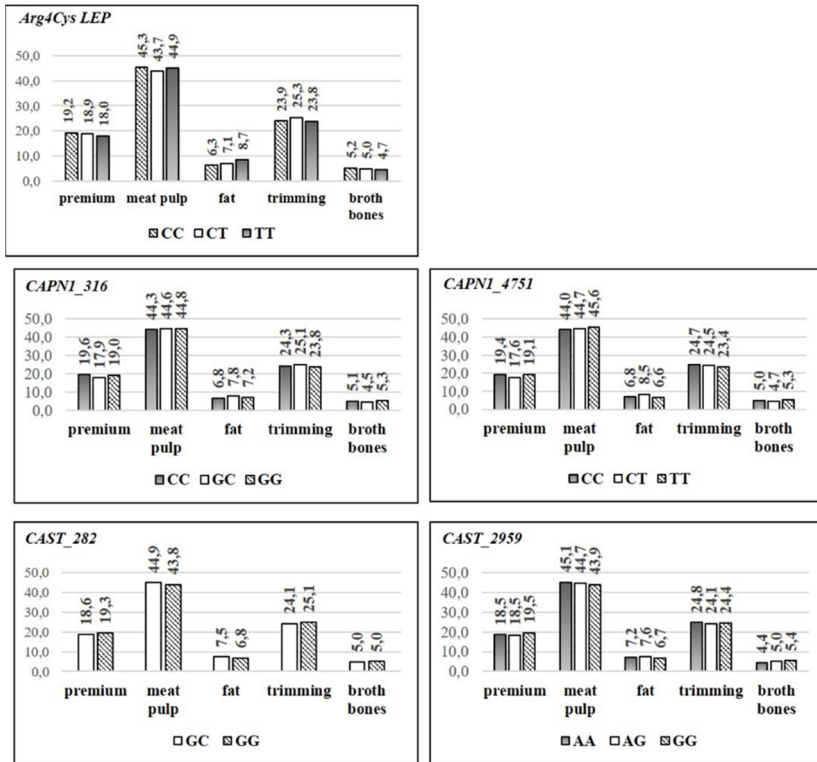


Fig. 1. Content of the different cuts in the Aberdeen Angus bulls' carcasses (%).

The evaluation of the total profit of carcasses has been conducted by summary of cost of valuable beef cuts (premium, meat pulp, fat and trimming, and broth bones). The results presented on Fig. 2 the columns of the best genotypes are shaded. As we proposed, the most profits have been obtained from the carcasses of animals of CC-Arg4Cys LEP, GG-CAPNI_316, TT-CAPNI_4751, GG-CAST_282 and GG-CAST_2959 genotypes.

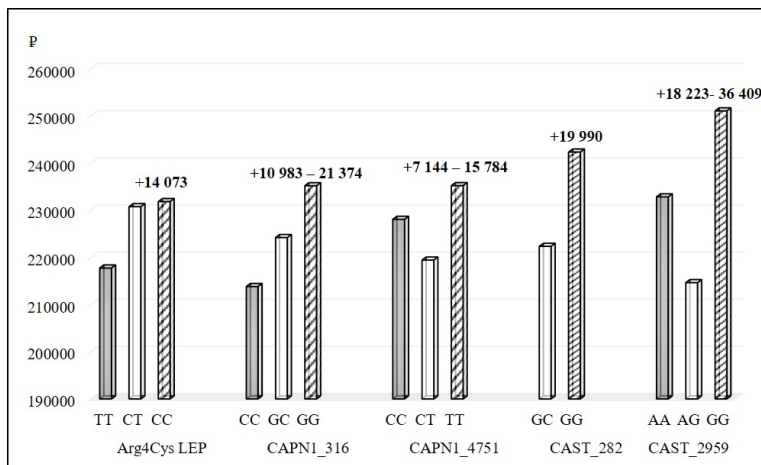


Fig. 2. The profit from the realization of the total carcass of Aberdeen Angus bulls of different LEP, CAPNI and CAST genotypes.

The profit from bulls of CC genotype of Arg4Cys *LEP* was more on 14 073 rubles compared TT-genotype-carriers. From the animals with genotype GG-*CAPNI_316* the profit was on 10 983-21 374 Rubles more compared with CC- and heterozygous genotypes. *CAPNI_4751* polymorphism has shown profitability of TT-genotype on 7 144-15 784 rubles more compared with another genotypes. On *CAST* polymorphisms the most profitable were genotypes GG-*CAST_282* (more 19 990 rubles) and GG-*CAST_2959* (more on 18 223-36 409 rubles).

4 Discussion

The previous investigations of gene polymorphisms associated with the meat quality traits have been conducted and the preferable alleles positively influenced on the beef productivity figures have been revealed [6, 7, 9, 10, 11 and 13]. In our previous works, established the relatively high frequencies of the desirable alleles of leptin and calpain 1 gene in the Russian populations of beef cattle [xx], we have observed the significant positive influence of allele T of Arg4Cys *LEP* polymorphism on animal fattening from born till wean [14, 15]. In the older age this discovered pattern has not been confirmed [xx]. We have also not find any influence of *CAPNI_316* polymorphism on average mass gains in Aberdeen Angus cattle [14] that allow propose more influence of calpain-calpastatin cascade genes on beef quality than on meat yield.

The results of the current work contradicted with the earlier proposes about the desirable alleles of the studies polymorphisms of leptin, calpain 1 and calpastatin genes. Despite of the beliefs that the alleles of T-Arg4Cys *LEP*, C-*CAPNI_316*, C-*CAPNI_4751*, C-*CAST_282* and A-*CAST_2959* are desirable in point of the productivity traits, the realization of beef from the bulls of homozygous on these alleles genotypes was less profit compared with ones from the animals homozygous on alleles C-Arg4Cys *LEP*, G-*CAPNI_316*, T-*CAPNI_4751*, G-*CAST_282* and G-*CAST_2959*. Probably the advantage in the profits obtained from realization of these beef has been observed due most content in the carcasses of the most valuable cuts (premium and meat pulp) and less content of fat and trimming, which are appropriate for the preparing of semi-finished products and so less expensive.

It must keep in mind that in the forming of the quality characteristics of meat happens under the influence as genetic as paratypical alive and after mortem factors, for example, animals managing, feeding and processes of slaughter, tenderization [3, 4]. In our opinion, in addition to study of the perspective genetic markers for the meat cattle breeding, the better understanding of the mechanism underlying in the realization of the animal genetic potential is needed.

5 Conclusion

Based on the obtained results we could conclude that using of the genetic markers of beef quality could facilitate to improve the its palatability characteristics but it is not obligatory will get the most profit. Moreover, in this point of review the increasing of the beef cattle profitability is most important than the increasing of its manufacturing volume.

Before the recommendation to practice implementation of some genetic markers, we must in addition to the largescale population and correlation investigations on the cattle to study of the mechanisms their realization on level of proteins that is possible by gene expression analysis. By only complex study would be possible to get true understanding of gene role in phenotype appearance of the traits and expediency of the using of some genetic markers in meat cattle breeding.

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